

Godbole, et al.

U.S. Application No. 09/756,247

AMENDMENTS TO THE SPECIFICATION

Please replace the existing paragraph beginning at page 12, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPITYVLQYLEKAGLLTEEIRSRAVGFLEIGYQKELM
YKHSNGSYSAFGERDGNNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS
GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKDVDDPMVSQGLRCLKNSAT
STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAISGESTYWSQKPTPSSNASPWSEPA
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNA YGGFSSTQDTVVALQAL
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of $4.4e-87$, protein database identification number entry = 1c3d [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 13, line 5, with the following rewritten paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSNMAIVEVKMLSGFSPM
EGTNQLLLQQPLVKKVEFGTDTLNIYLDLIKNTQTYTFTISQSVLVTNLKPATIKVYDY
YLPGSFKLSQYTTIVWSMNND

(designated as SEQ ID NO: 22) with PSI-BLAST e-value of $4.4e-52$, protein database identification number entry = 1bv8 [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 1349-1479 of SEQ ID NO: 4.--

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Please replace the existing paragraph beginning at page 134, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTEEIRSRAVGFLEIGYQKELM
YKHSNGSYSAFGERDGNNGNTWLTAFTVKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS
GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKD VDDPMVSQGLRCLKNSAT
STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAUSGESIYWSQKPTPSSNASPWSEPA
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNA YGGFSSTQDTVVALQAL
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of 4.4e-87, protein database identification number entry = 1c3d [Research collaboratory for Structural Bioinformatics. ~~Berman et al., Nucl. Acids Res. 28:235-242 (2000)~~], verify score = 0.49, located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 135, line 8, with the following rewritten paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSSNMAIVEVKMLSGFSPM
EGTNQLLLQQPLVKKVEFGTDTLNTYLDLIKNTQTYTFTISQSVLVTNLKPATIKVYDY
YLPGSFKLSQYTIVWSMNDS

(designated as SEQ ID NO: 22) with PSI-BLAST e-value of 4.4e-52, protein database identification number entry = 1bv8 [Research collaboratory for Structural Bioinformatics. ~~Berman et al., Nucl. Acids Res. 28:235-242 (2000)~~], verify score = 0.49, located at residues 1349-1479 of SEQ ID NO: 4.--